

SeqServer
biology in silico**BLAST2 Search Results**

Sequences

Help

Retrieval

BLAST2

FASTA

ClustalW

GCC Assembly

Phrap

Translation

BLAST2 Manual

Confidential -- Property of Incyte Genomics, Inc. SeqServer Version 4.6 March 2001

Program: blastp**Sequence ID(s):**☐ PF-0459US_SEQIDNO:25/102 vs. genpept122

NCBI-BLASTP 2.0.10 [Aug-26-1999]



Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= PF-0459US_SEQIDNO:25/102
(150 letters)

Database: genpept122
698,042 sequences; 216,183,515 total letters

Searching.....done

Sequences producing significant alignments:

Score E
(bits) Value

<input checked="" type="checkbox"/>	g2388627	chemokine [Homo sapiens]	307	7e-83
<input checked="" type="checkbox"/>	g5881909	thymus-expressed chemokine [Mus musculus]	127	7e-29
<input checked="" type="checkbox"/>	g2388629	chemokine [Mus musculus]	125	2e-28
<input checked="" type="checkbox"/>	g6561400	CC chemokine 6Ckine-leu [Mus musculus]	48	6e-05
<input checked="" type="checkbox"/>	g12025212	small inducible cytokine A21c [Mus musculus]	48	6e-05
<input checked="" type="checkbox"/>	g12025210	small inducible cytokine A21b [Mus musculus]	48	6e-05
<input checked="" type="checkbox"/>	g3169697	beta chemokine Exodus-2 [Mus musculus]	48	8e-05
<input checked="" type="checkbox"/>	g6561402	CC chemokine 6Ckine-ser [Mus musculus]	46	3e-04
<input checked="" type="checkbox"/>	g3947924	TCA4 [Mus musculus]	46	3e-04
<input checked="" type="checkbox"/>	g2624927	beta chemokine [Mus musculus]	46	3e-04
<input checked="" type="checkbox"/>	g2209189	TCA4 [Mus musculus]	46	3e-04
<input checked="" type="checkbox"/>	g12025208	small inducible cytokine A21a [Mus musculus]	46	3e-04
<input checked="" type="checkbox"/>	g6456876	thymic stroma chemokine-1 precursor [Homo sapiens]	45	4e-04
<input checked="" type="checkbox"/>	g5921131	chemokine eotaxin3 [Homo sapiens]	45	4e-04
<input checked="" type="checkbox"/>	g5669887	CC chemokine IMAC [Homo sapiens]	45	4e-04
<input checked="" type="checkbox"/>	g4539796	small inducible cytokine subfamily A member 26 [Homo	45	4e-04
<input checked="" type="checkbox"/>	g4263736	similar to cytokines; similar to A31767 (PID:g88665)	45	4e-04

<input checked="" type="checkbox"/>	g4128129	secondary lymphoid tissue chemokine [Homo sapiens]	43	0.003
<input checked="" type="checkbox"/>	g2624925	beta chemokine [Homo sapiens]	43	0.003
<input checked="" type="checkbox"/>	g2335035	SLC [Homo sapiens]	43	0.003

Database: genpept122

Posted date: Mar 1, 2001 9:38 AM

Number of letters in database: 216,183,515

Number of sequences in database: 698,042

Lambda	K	H
0.322	0.133	0.419

Gapped

Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 62235040

Number of Sequences: 698042

Number of extensions: 2321593

Number of successful extensions: 6166

Number of sequences better than 10.0: 163

Number of HSP's better than 10.0 without gapping: 32

Number of HSP's successfully gapped in prelim test: 131

Number of HSP's that attempted gapping in prelim test: 6120

Number of HSP's gapped (non-prelim): 164

length of query: 150

length of database: 216,183,515

effective HSP length: 51

effective length of query: 99

effective length of database: 180,583,373

effective search space: 17877753927

effective search space used: 17877753927

T: 11

A: 40

X1: 16 (7.4 bits)

X2: 38 (14.8 bits)

X3: 64 (24.9 bits)

S1: 41 (22.0 bits)

Submit sequences to:



SeqServer
biology in silico

BLAST2 Search Results

Sequences

Help

Retrieval

BLAST2

FASTA

ClustalW

GCG Assembly

Phrap

Translation

BLAST2 Manual

Confidential -- Property of Incyte Genomics, Inc. SeqServer Version 4.6 March 2001

Program: blastp**Sequence ID(s):**

☐ PF-0459US_SEQIDNO:25/102 vs. genpept122

NCBI-BLASTP 2.0.10 [Aug-26-1999]



Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= PF-0459US_SEQIDNO:25/102
(150 letters)

Database: genpept122
698,042 sequences; 216,183,515 total letters

Searching.....done

Sequences producing significant alignments:

Score E
(bits) Value

<input checked="" type="checkbox"/> <u>g2388627</u>	chemokine [Homo sapiens]	307	7e-83
<input checked="" type="checkbox"/> <u>g5881909</u>	thymus-expressed chemokine [Mus musculus]	127	7e-29
<input checked="" type="checkbox"/> <u>g2388629</u>	chemokine [Mus musculus]	125	2e-28

>g2388627 chemokine [Homo sapiens]
Length = 150

Score = 307 bits (777), Expect = 7e-83
Identities = 147/150 (98%), Positives = 147/150 (98%)

```

Query: 1  MNLWLLACLVAGFLGAWAPAVHAQG VFEDCC LAYHYPIGWAVLRR AWTYRIQEVSGSCNL 60
          MNLWLLACLVAGFLGAWAPAVH QGVFEDCC LAYHYPIGWAVLRR AWTYRIQEVSGSCNL
Sbjct: 1  MNLWLLACLVAGFLGAWAPAVHTQGVFEDCC LAYHYPIGWAVLRR AWTYRIQEVSGSCNL 60

Query: 61 PAAIFYLPKRHRKVCGNPKSREVQ RAMKLLDARNKVF AKLRHNTQT FQAGPHAVKKLSSG 120
          PAAIFYLPKRHRKVCGNPKSREVQ RAMKLLDARNKVF AKL HN QTFQAGPHAVKKLSSG
Sbjct: 61 PAAIFYLPKRHRKVCGNPKSREVQ RAMKLLDARNKVF AKLHHNMQTFQAGPHAVKKLSSG 120

Query: 121 NSKLSSSKFSNPISSSK RNVSL LISANSGL 150
          NSKLSSSKFSNPISSSK RNVSL LISANSGL
Sbjct: 121 NSKLSSSKFSNPISSSK RNVSL LISANSGL 150

```

>g5881909 thymus-expressed chemokine [Mus musculus]
Length = 144

Score = 127 bits (316), Expect = 7e-29

Identities = 71/143 (49%), Positives = 87/143 (60%), Gaps = 14/143 (9%)

Query: 1 MNLWLLACLVAGFLGAWAPAVHAQGVFEDCCLAYHYPIGWAVLRRRAWTYRIQEVSGSCNL 60
M LWL ACLVA F+GAW P VHAQG FEDCCL Y + I W VLR A Y QEVS GSCNL
Sbjct: 1 MKLWLFACLVACFVGAWMPVVHAQGAFEDCCLGYQHRIKWNVLRHARNYHQEVSGSCNL 60

Query: 61 PAAIFYLPKRHRKVCGNPKSREVQRAMKLLDARNK-VFAKLRHNTQTTFQAGPHAVKKLSS 119
A FY R + VCGNP+ V+RAM++L AR + V K ++QT + + +K
Sbjct: 61 RAVRFYF--RQKVVCGNPEDMNVKRAMRILTARKRLVHWKSASDSQTERKKS NHMK----- 114

Query: 120 GNSKLSSSKFSNPISSSKRNVSL 142

SK NP S+S R+ +L

Sbjct: 115 -----SKVENPNSTSVRSATL 130

>g2388629 chemokine [Mus musculus]
Length = 144

Score = 125 bits (312), Expect = 2e-28

Identities = 70/143 (48%), Positives = 87/143 (59%), Gaps = 14/143 (9%)

Query: 1 MNLWLLACLVAGFLGAWAPAVHAQGVFEDCCLAYHYPIGWAVLRRRAWTYRIQEVSGSCNL 60
M LWL ACLVA F+GAW P VHAQG FEDCCL Y + I W VLR A Y QEVS GSCNL
Sbjct: 1 MKLWLFACLVACFVGAWMPVVHAQGAFEDCCLGYQHRIKWNVLRHARNYHQEVSGSCNL 60

Query: 61 PAAIFYLPKRHRKVCGNPKSREVQRAMKLLDARNK-VFAKLRHNTQTTFQAGPHAVKKLSS 119
A FY R + VCGNP+ V+RA+++L AR + V K ++QT + + +K
Sbjct: 61 RAVRFYF--RQKVVCGNPEDMNVKRAIRILTARKRLVHWKSASDSQTERKKS NHMK----- 114

Query: 120 GNSKLSSSKFSNPISSSKRNVSL 142

SK NP S+S R+ +L

Sbjct: 115 -----SKVENPNSTSVRSATL 130

Database: genpept122

Posted date: Mar 1, 2001 9:38 AM

Number of letters in database: 216,183,515

Number of sequences in database: 698,042

Lambda	K	H
0.322	0.133	0.419

Gapped Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 62235040

Number of Sequences: 698042

Number of extensions: 2321593

Number of successful extensions: 6166

Number of sequences better than 10.0: 163

Number of HSP's better than 10.0 without gapping: 32

Number of HSP's successfully gapped in prelim test: 131

Number of HSP's that attempted gapping in prelim test: 6120

Number of HSP's gapped (non-prelim): 164

length of query: 150

length of database: 216,183,515

effective HSP length: 51

effective length of query: 99
effective length of database: 180,583,373
effective search space: 17877753927
effective search space used: 17877753927
T: 11
A: 40
X1: 16 (7.4 bits)
X2: 38 (14.8 bits)
X3: 64 (24.9 bits)
S1: 41 (22.0 bits)

[Graphical Viewer...](#)

Submit sequences to:

